

FIG. 1A

1	CCCACGCGTCCGATTAAAGTGAGGAGAGAGCTACAACCAAGTAAGCAAGTGTCAGGGCTC	60
61	ACCAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTGTTC	120
1	<u>M O G O G R R R G T C K D I F C S K</u>	18
121	AATGGCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTG	180
19	<u>M A S Y L Y G V L F A V G L C A P I Y C</u>	38
181	TGTGTCCCCGGCCAATGCCCCAGTGCATACCCCCGCCCTTCCTCCACAAAGAGCACCCC	240
39	V S P A N A P S A Y P R P S S T K S T P	58
241	TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGGT	300
59	A S Q V Y S L N T D F A F R L Y R R L V	78
301	TTTGGAGACCCGAGTCAGAACATCTTCTCTCCCCTGTGAGTGTCTCCACTTCCCTGGC	360
79	L E T P S Q N I F F S P V S V S T S L A	98
361	CATGCTCTCCCTTGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTT	420
99	M L S L G A H S V T K T Q I L Q G L G F	118
421	CAACCTCACACACACACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTC	480
119	N L T H T P E S A I H Q G F Q H L V H S	138
481	ACTGACTGTTCCCAGCAAAGACCTGACCTTGAAGATGGGAAGTGGCCTCTTCGTCAAGAA	540
139	L T V P S K D L T L K M G S A L F V K K	158
541	GGAGCTGCAGCTGCAGGCAAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGT	600
159	E L Q L Q A N F L G N V K R L Y E A E V	178
601	CTTTTCTACAGATTTCTCCAACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAA	660
179	F S T D F S N P S I A Q A R I N S H V K	198
661	AAAGAAGACCCAAGGGAAGGTTGTAGACATAATCCAAGGCCTTGACCTTCTGACGGCCAT	720
199	K K T Q G K V V D I I Q G L D L L T A M	218
721	GGTTCTGGTGAATCACATTTTCTTTAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGAATA	780
219	V L V N H I F F K A K W E K P F H L E Y	238
781	TACAAGAAAGAACTTCCCATTCCTGGTGGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT	840
239	T R K N F P F L V G E Q V T V Q V P M M	258
841	GCACCAGAAAGAGCAGTTCGCTTTTGGGGTGGATACAGAGCTGAACTGCTTTGTGCTGCA	900
259	H Q K E Q F A F G V D T E L N C F V L Q	278

FIG. 1B

901 GATGGATTACAAGGGAGATGCCGTGGCCTTCTTTGTCCTCCCTAGCAAGGGCAAGATGAG 960
 279 M D Y K G D A V A F F V L P S K G K M R 298
 961 GCAACTGGAACAGGCCTTGTCAGCCAGAACACTGATAAAGTGGAGCCACTCACTCCAGAA 1020
 299 Q L E Q A L S A R T L I K W S H S L Q K 318
 1021 AAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCCATTTCTGCCTCCTACAATCTGGAAAC 1080
 319 R W I E V F I P R F S I S A S Y N L E T 338
 1081 CATCCTCCCGAAGATGGGCATCCAAAATGCCTTTGACAAAAATGCTGATTTTTCTGGAAT 1140
 339 I L P K M G I Q N A F D K N A D F S G I 358
 1141 TGCAAAGAGAGACTCCCTGCAGGTTTCTAAAGCAACCCACAAGGCTGTGCTGGATGTCAG 1200
 359 A K R D S L Q V S K A T H K A V L D V S 378
 1201 TGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAGTTCATAGTCCGATCGAAGGA 1260
 379 E E G T E A T A A T T T K F I V R S K D 398
 1261 TGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCTGATGATGATTACAAATAA 1320
 399 G P S Y F T **V S F N R T F L M M I** T N K 418
 1321 AGCCACAGACGGTATTCTCTTTCTAGGGAAAGTGGAAAAATCCCACTAAATCCTAGGTGGG 1380
 419 A T D G I L F L G K V E N P T K S * 436
 1381 AAATGGCCTGTTAAGTATGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCT 1440
 1441 CTTTCTGTTCTGAGGGTGCATTTGACCCCAGTGGAGCTGGATTGCTGGCAGGGATGCCA 1500
 1501 CTTCCAAGGCTCAATCACCAAAACCATCAACAGGGACCCCAGTCACAAGCCAACACCCATT 1560
 1561 AACCCAGTCAGTGCCCTTTTCCACAAATTCTCCAGGTAAGTACTAGCTTCATGGGATGTTG 1620
 1621 CTGGGTTACCATATTTCCATTCTTGGGGCTCCAGGAATGGAAATACGCCAACCCAGGT 1680
 1681 TAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAACTAAAAATATGAAAAAAA 1740
 1741 AAAAAAAAAAAAAAAAAAAAAAAAAA 1766

FIG. 2

	1	50
AL132708_FL	(1) MQGQRRRGTCCKDIFCSKMASYLYGVLEFAVGLCAPIYCVSPANAPSAYPR	
AACT_HUMAN	(1) -----MERMLPLALGLLAAGFCPAVLCHPNSPLD	
KAIN_HUMAN	(1) -----MHLIDYLLELLVGLLALSHGQLHVEHDGESCS	
THBG_HUMAN	(1) -----MSPFLYLVLVLGLHATIHCAASPEGKVTACHS	
	51	100
AL132708_FL	(51) PS-----STKSTPASQVYSLNTDEAFRLYRRLVLETSPQNIFESPVS	
AACT_HUMAN	(31) EENLTQENQDRGTHVDLGLASANVDAFSLYKQLVLKAPDKNVIESPLSI	
KAIN_HUMAN	(33) NSSHQILETGEGSPSLKIAPANADFAFRFYLIASETPGKNIFFSPLSI	
THBG_HUMAN	(33) -----SQPNATLYKMSSINADFAFNLYRRFTVETPDKNIFFSPVSI	
	101	150
AL132708_FL	(94) STSLAMLSLGAHSVTKQTLLQGLGFNLHTHPESAIHQGFQHLVHSETVPS	
AACT_HUMAN	(81) STALAFSLGAHNTTLTEILKGLKRNLTETSEAEIHQSFOHLLRTINQSS	
KAIN_HUMAN	(83) SAAYAMLSLGACSHSRSQILEGLGFNLTELSSESDVHRGFQHLHTNLPG	
THBG_HUMAN	(74) SAALVMLSFGACCSQTQTEIVETLGFNLTDTPMVEIQHGFQHLICSLNFPK	
	151	200
AL132708_FL	(144) KDETLKMGSALFVKKEQLQANFLGNVKRLYEAEVFSTDESNPISIAQART	
AACT_HUMAN	(131) DELQLSMGNAMFVKEQLSLDRFTEDAKRLYGSEAFATFDQDSAAAKKLI	
KAIN_HUMAN	(133) HGLETRVGSALFLSHNLKFLAKFLNDTMAVYEAKLFHTNFYDVTGTIQLI	
THBG_HUMAN	(124) KELELQIGNALEFIGKHLKPLAKFLNDVKTLYETEVEFSTDESNISAAKQEI	
	201	250
AL132708_FL	(194) NSHVKKKTQCKVVDIIQGLDLLTAMVLVNHIFKAKWEKPFHLEYTRKNF	
AACT_HUMAN	(181) NDYVKNGTGKITDILKDLDSQTMVLVNYIFKAKWEMPFDPQDTHQSR	
KAIN_HUMAN	(183) NDHVKKETRGKIVDLVSELKKDVLMLVNYTYFKALWEKPFISSRTTPKD	
THBG_HUMAN	(174) NSHVEMQTKGKVGLIQDLKPNTIMVLVNYIHFKAQWANPFDPSTEDSS	
	251	300
AL132708_FL	(244) PFLVGEQVTVQVPMMHQKEQFAFGVDTELNCFVLQMDYKGDVAFFVIPS	
AACT_HUMAN	(231) FYLSKKKWVMVPMMSLHHLTIPYFRDEELSCTVVELKYTGNASALEIIPD	
KAIN_HUMAN	(233) FYVDENTTVRVPMMLQDQEHHWYLDHRYLPCSVLRMDYKGDATVFVILPN	
THBG_HUMAN	(224) SFLIDKTTTVQVPMMHQMEQYHYLVDMELNCTVLQMDYKSNALALEVLPK	
	301	350
AL132708_FL	(294) KGKMRQLEQALSARTLIKWSHSLQKR---WIEVFIPRESISASYNLETI	
AACT_HUMAN	(281) QDKMEEVEAMLLPETLKRWRDSLEFR---EIGELYLPKFSISRDNINDI	
KAIN_HUMAN	(283) QGKMREIEEVLTPPEMLMRWNNLLRKRNFYKKLELHLPKFSISGSYVLDQI	
THBG_HUMAN	(274) EGQMESVEAAMSSKTLKKWNRLQKG---WVDLFVPKFSISATYDLGAT	
	351	400
AL132708_FL	(340) LPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATT	
AACT_HUMAN	(328) LLQLGIEEAFTSKADLSGITGARNLAVSQVHHKAVLDVFEEGTEASAATA	
KAIN_HUMAN	(333) LPRLGFTDLFSKWADLSGITKQOKLEASKSFHKATLDVDEAGTEAAAATT	
THBG_HUMAN	(320) LLKMGIQHAYSENADFSLTEDNGLKLSNAAHKAVLHIGKGEAAAVPE	
	401	446
AL132708_FL	(390) TKFIVRSKDGPSYFTVSNRTFLMMITNKATDGILFLGKVENPTKS	
AACT_HUMAN	(378) VKITLLSALVETRRTIVRFNRPELMIIVPTDTONIFFMSKVTNPKQA	
KAIN_HUMAN	(383) FAIKFFSAQTN-RHILRFNRPELVVIFSTSTQSVLEFLGKVVDETKP	
THBG_HUMAN	(370) VELSDQPENTFLHPIIQIDRSFMLLILERSTRSILFLGKVVNPTKA	

↓↓↓↓↓↓↓↓↓↓

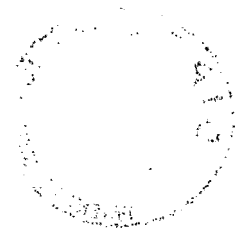


FIG. 3

LSI-01 pdblqlp	MQGQGRRRGT CKDIFCSKMA SYLYGVLFV GLCAPIYCVS PANAPSAYPRMDPQ GDAAQKTDTS
LSI-01 pdblqlp	PSSTKSTPAS QVYSLNTDFA FRLYRREVLV TPSQNIFFSP VSVSESLAME HHDQDHPTFN KITPNLAEPF FSLYRQAAHQ SNSTNREFSP VSIAMAFAML
LSI-01 pdblqlp	SLGAHSVETK QELQSGENL THTDESATHQ GQGHVHSET VPSKDETHKM SLGTKADTHD ETEGENFNL TEIPRAQHEH GQGHLLRTEN QDSDQEQHTT
LSI-01 pdblqlp	GSALFVKKEL QLQANFLGNV KRLYEAEVFS TDESNPISIAQ ARENSHVKKK GNGLFLSEGL KLVDKEDVDV KGLVHSEAFV VNEGDTEAK KQNDYMEKG
LSI-01 pdblqlp	TQGVVDIIQ GLDLLTAMVL VNHFFRAKW EKPFHLEYTR KNFPFLVGEQ TQGVVDLVK ELDRTVFAV VNYFFRGKW ERPFVVKDT. EEEDFHVQV
LSI-01 pdblqlp	VTQVPMHQ KEQAFGVDT ELNCFVLQMD YKGDVAFFV LPSKGMROE TVKVPMMKR LGMFNHQCK KLSWVLLMK YLGNATAIF LPEQNLQHL
LSI-01 pdblqlp	EQALSARTLI KWSHSLQKW IEVFIPRFSI SASYNLETIL PKMGTQNAED ENELTHDIIT KPLENEDRRS ASLHLPKLSI TGTDEKSVL GQLGITKVS
LSI-01 pdblqlp	KNADFSGIK RDSLQVSKAT HKAVIDVSEE GTEATAATTT KFEVRSKGGP NGADLSGVTE EAPKLSKAV HKAVIDIDEK GTEAAGAMFL EATFMSI..P
LSI-01 pdblqlp	S.YFTVSFNR TFLMMITNKA TDGILFLGKV ENPTKS PE...VKFNK PVVFLMIEQN TKSPFLMGKV VNPTOK

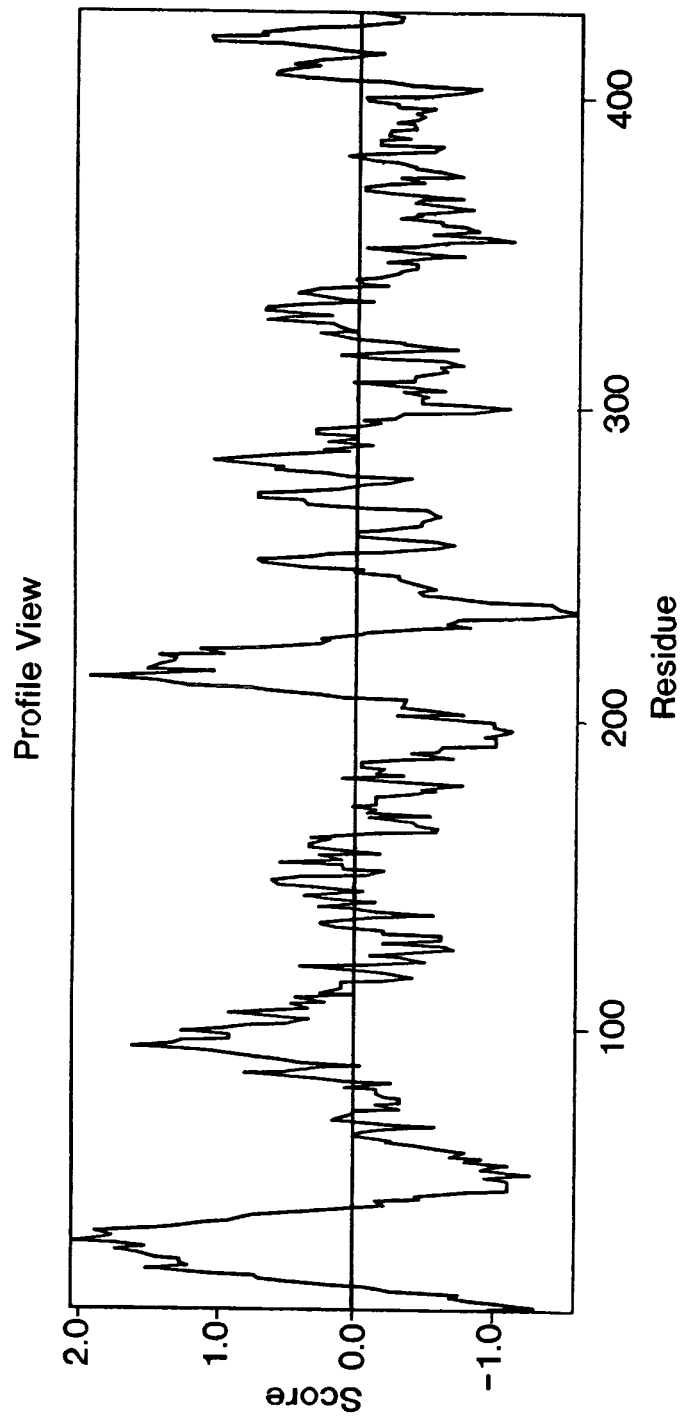
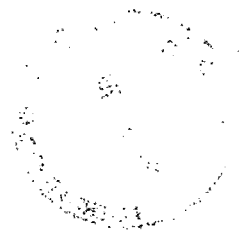


FIG. 4



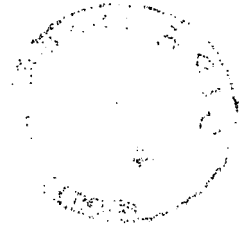


FIG. 5A

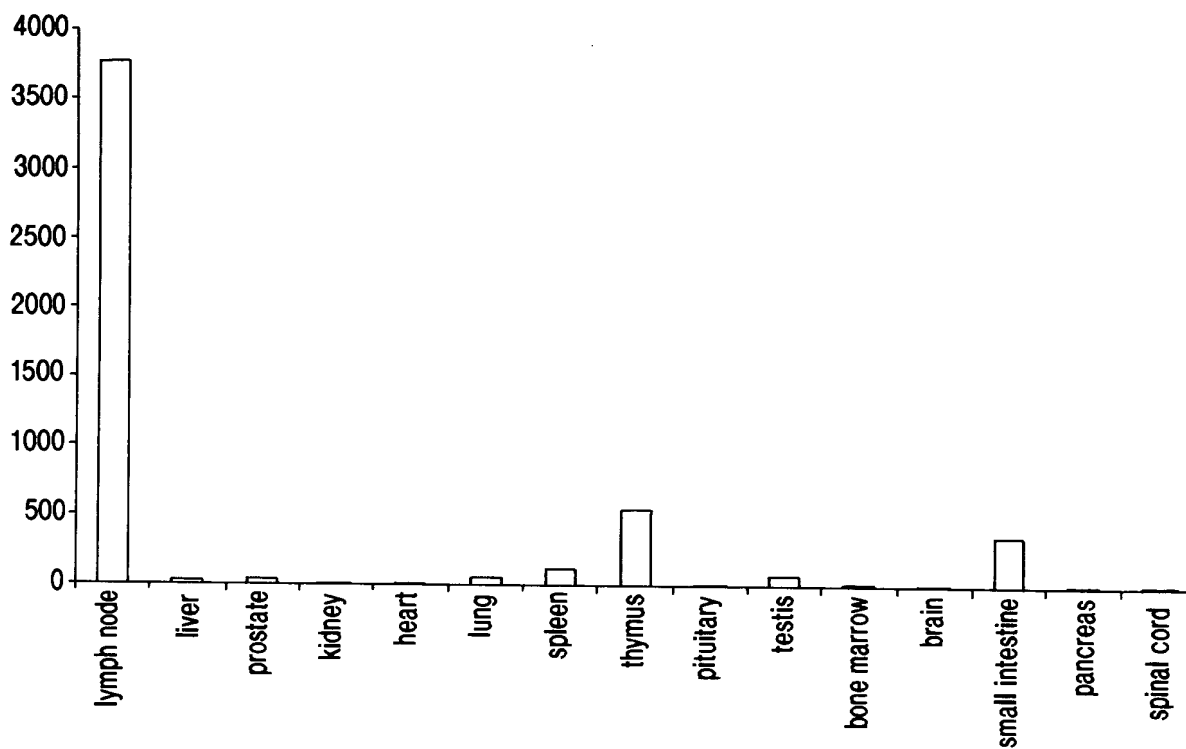
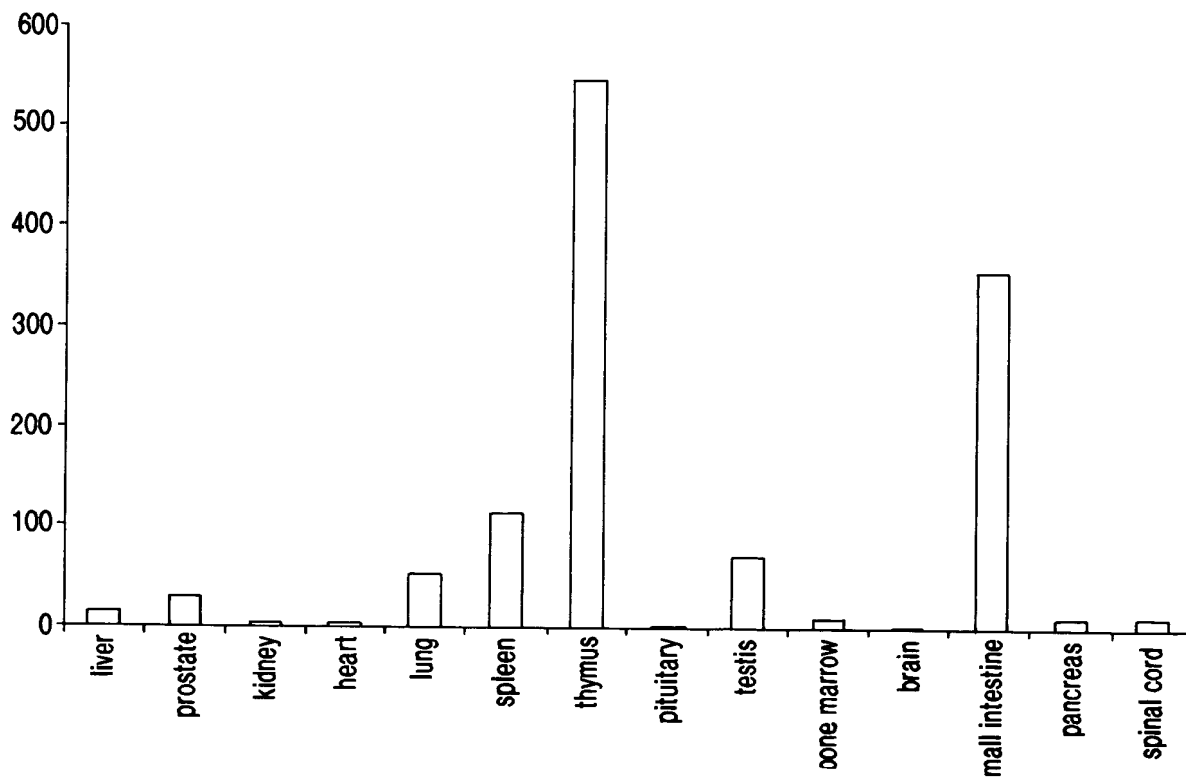


FIG. 5B



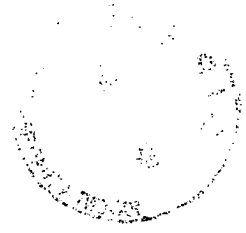


FIG. 6

Protein	Genbank ID	Identities	Similarities
human α_1 -antichymotrypsin	gi 112874	46%	52%
human Kallistatin	gi 5453888	48%	56%
human thyroxin-binding globulin	gi 37142	51%	57%
human α_1 -antithrypsin	gi 6137432	43%	50%

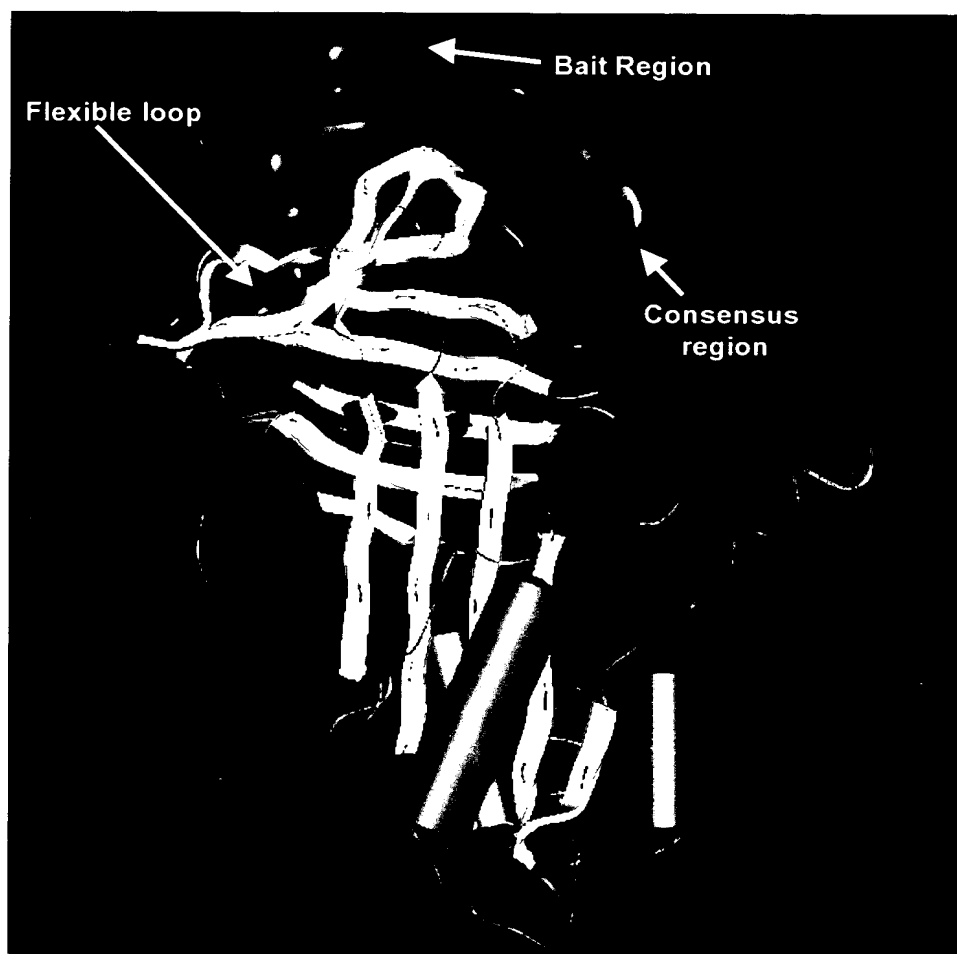


FIG. 7